



Bovine-Specific Nucleotide Polymorphisms and mRNA Expression of the Growth Hormone Secretagogue Receptor 1a (*GHSR1a*) Gene and its Genetic Association with Growth and Carcass Traits

Masanori Komatsu^{1*}, Yoichi Sato², Yuki Fujimori³, Tomohito Itoh⁴, Masahiro Satoh¹, Motohide Nishio¹, Osamu Sasaki¹, Hideaki Takahashi¹ and Aduli EO Malau-Aduli⁵

¹NARO Institute of Livestock and Grassland Science, National Agriculture and Food Research Organization (NARO), Tsukuba, Ibaraki, Japan

²Animal Industry Research Institute, Iwate Prefecture Livestock Research Centre, Takizawa, Japan

³Nagano Prefecture Livestock Research Centre, Shiojiri, Japan

⁴Maebashi Institute of Animal Science, Livestock Improvement Association of Japan, Inc. (LIAJ), Maebashi, Japan

⁵Animal Science & Genetics, Tasmanian Institute of Agriculture, School of Land and Food, University of Tasmania, Hobart, Tasmania, and School of Veterinary & Biomedical Sciences, Faculty of Medicine, Health & Molecular Sciences, James Cook University, Townsville, Queensland, Australia

*Corresponding author: Masanori Komatsu, Animal Breeding and Genetics Research Group, NARO Institute of Livestock and Grassland Science, National Agriculture and Food Research Organization (NARO), Tsukuba, Ibaraki 305-0901, Japan, Tel: (+81)-29-838-8614; Fax: (+81)-29-838-8623; E-mail: mkomatsu@affrc.go.jp

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Abstract

The growth hormone secretagogue receptor 1a (*GHSR1a*) is involved in many important functions including growth hormone (GH) secretion and appetite regulation and other important functions. We reveal herein, the unravelling of bovine-specific 5'untranslated region (5'UTR) microsatellite polymorphisms, a 3bp-indel in exon 1 (*DelR242*) and two different kinds of transcripts of the *GHSR1a* gene (spliced, without a microsatellite within the 5'UTR (*GHSR1a*); and non-spliced, with the microsatellite (*GHSR1b*)). A number of 17 alleles ((*TG*)₁₀₋₃₃) in the 5'UTR microsatellite was found in 11 cattle breeds. Furthermore, we found the *DelR242* (3R) allele, a truncated 3-arginine residue (3R) (major type: 4 arginine residues (4R)) within the intracellular loop 3 of *GHSR1a* protein in Japanese Shorthorn with a high frequency of 0.43 compared to the low frequency of 0.00~0.09 in other cattle breeds. We carried out a genetic association study between the 5'UTR microsatellite and growth and carcass traits in 1,285 steers. Statistical analysis revealed that the 5'UTR microsatellite locus had a significant additive effect on carcass weight (CW) and average daily gain (ADG). The 19-TG allele had a significantly desirable effect on these traits. We proposed a translational hypothesis that the association is due to differences in the secondary structure of *GHSR1b* mRNA among the *GHSR1a* gene haplotypes. We also examined age-related changes in the expressions of *GHSR1a* and *GHSR1b* in many cattle tissues. The *GHSR1a* mRNA expression in the arcuate nucleus of post-weaning calves was more than 10-fold higher than those of pre-weaning calves and cows. In peripheral tissues, there were 3 marked differences in mRNA expression between cattle, humans and mice, as follows: (1) the *GHSR1a* mRNA expression in the liver is high in cattle and very low in humans and mice; (2) the *GHSR1b* mRNA expression in the liver is low in cattle and high in humans; (3) the *GHSR1b* mRNA expression in the pancreas is very high in cattle.

Keywords: Ghrelin Receptor (*GHSR*); Microsatellite; *DelR242*; mRNA expression; mRNA secondary structure; Growth and carcass traits; Cattle

Bovine-Specific Nucleotide Polymorphisms of the *GHSR1a* Gene and Its Genetic Association with Growth and Carcass Traits

The growth hormone secretagogue receptor 1a (*GHSR1a*), also known as ghrelin receptor, is involved in many important functions including growth hormone (GH) secretion, appetite regulation, energy balance and other important functions [1,2]. In cattle, the *GHSR1a* gene was reported as a potential candidate gene when we detected growth trait QTLs in Japanese Black cattle using microsatellite DNA markers and half-sib regression analysis [3]. With respect to the bovine *GHSR1a* gene, it is of great interest that a polymorphic microsatellite ((*TG*)_n) is located within the 5'-flanking region of this locus [4], because no microsatellite had ever been found within the *GHSR1a* locus in either humans [5], mice [6] or rats [7]. However,

there was no published report on nucleotide polymorphisms from the 5'-flanking region to the 3'-UTR nor on the transcriptional analysis of the 5'-UTR of the *GHSR1a* gene in cattle. Therefore, we revealed for the first time, novel nucleotide polymorphisms from the 5'-flanking region to the 3'UTR (~6 kb) and two different kinds of transcripts (spliced, without a microsatellite within 5'UTR (*GHSR1a*); and non-spliced, with the microsatellite (*GHSR1b*)) of the bovine *GHSR1a* gene (Figure 1) [8]. The nucleotide sequencing of this gene (~6 kb) revealed 47 single nucleotide polymorphisms (SNPs), 4 indels and the two microsatellites ((*TG*)_n) in 5'UTR and (*GTTT*)_n in Intron 1). A number of 17 alleles (10-TG to 33-TG) was found in the 5'UTR microsatellite locus in 11 cattle breeds. There were breed differences in allele frequencies and major alleles. Specifically, in Japanese Black cattle, the major alleles were 19-TG, 23-TG and 24-TG; alleles 19-TG, 21-TG, 22-TG, 23-TG and 24-TG in European cattle breeds, and alleles 10-TG and 22-TG in Philippine native cattle breeds (a mixture of *Bos indicus* and *Bos taurus* types). Short repeat number alleles 10-TG, 15-TG, 16-TG and 18-TG were found in the Philippine native cattle. The microsatellite TG-repeat sequences included one

cytosine(C) instead of guanine (G) at the 9th repeat position from the 3'-end of this locus of 7 alleles ($((TG)_{10-24} TC)(TG)_8$). This position was constant and independent of the TG-repeat number. These results suggest that the TG-repeat number of microsatellites increased with evolution from the 3'-end to the 5'-end direction of this sequence (Figure 1).

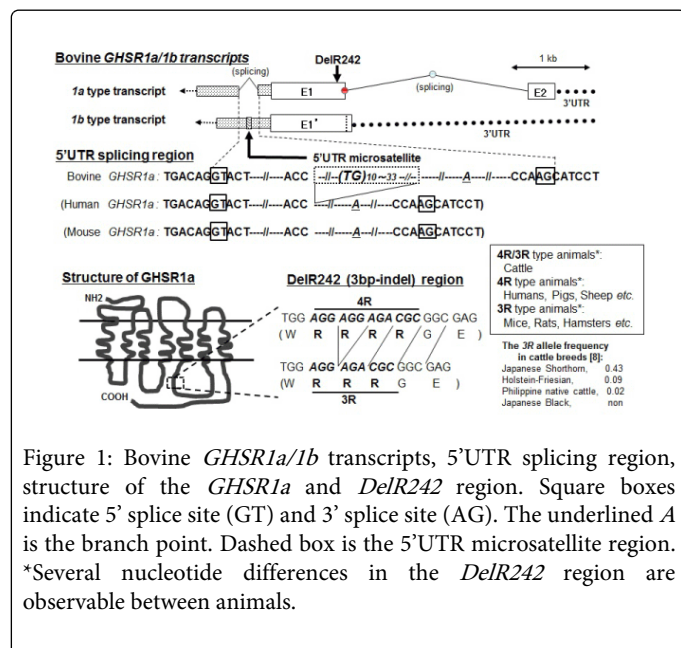


Figure 1: Bovine *GHSR1a/1b* transcripts, 5'UTR splicing region, structure of the *GHSR1a* and *DelR242* region. Square boxes indicate 5' splice site (GT) and 3' splice site (AG). The underlined A is the branch point. Dashed box is the 5'UTR microsatellite region. *Several nucleotide differences in the *DelR242* region are observable between animals.

We investigated the genetic association between the 5'UTR microsatellite ($((TG)_n)$) of the *GHSR1a* gene and growth and carcass traits in Japanese Black cattle [9]. We used a population of 1,285 Japanese Black steers in a progeny-testing program of the Livestock Improvement Association of Japan (LIAJ). Genetic association analysis between DNA markers, growth and carcass traits was carried out using a univariate model within the framework of a derivative-free restricted maximum likelihood algorithm as applied in the MTDFREML [10]. MTDFREML statistical analysis clearly revealed that the 19-TG allele, one of the four major microsatellite alleles, had a very significant additive substitution effect on carcass weight (CW) ($P < 0.0007$), and average daily gain (ADG) ($P < 0.0002$). Besides, the A allele of the *nt-7(C>A)* locus also had a significant effect on these traits (CW: $P < 0.002$; ADG: $P < 0.05$). To further investigate the combined effect of both the 5'UTR microsatellite ($((TG)_n)$) and *nt-7(C>A)* on these traits, haplotypes of the 5'UTR microsatellite ($((TG)_n)$) and the *nt-7(C>A)* were constructed and statistically analyzed. The results demonstrated that the [19-TG]-[A] haplotype had the most significant additive effect on these growth and carcass traits.

It has been reported that GT repeat polymorphisms in *Tilapia* prolactin 1 (*prl 1*) 5'UTR promoter are associated with differences in *prl 1* gene expression and the growth response of salt-challenged fishes [11]. The length of the TG-repeat in the P1 promoter region of the growth hormone receptor (*GHR*) gene was significantly related to growth and carcass traits in beef cattle [12,13]. Stepwise increase in repeat numbers from 0 to 21 for a CA-microsatellite located in the promoter of the human matrix metalloproteinase-9 gene has been reported to produce incremental surges in transcription rates [14]. Furthermore, a review of the simple sequence repeats (SSRs) in the 5'-UTR by Li *et al.* [15] revealed that the regulation of gene expression is affected by both transcription and translation. Therefore, a logical

explanation for the association between 5'UTR microsatellite ($((TG)_n)$) polymorphism and growth traits is through differences in transcriptional or splicing or translational levels of the *GHSR1a* gene. The first, a "transcriptional hypothesis" is that the differences in DNA structure around the 5'UTR microsatellite region between [19-TG] and [non-19-TG] simultaneously affect transcriptional levels of both the 1a and 1b mRNAs from the 1a gene. However, this hypothesis is hard to explain using the *GHSR1b* function because it has been reported that *GHSR1b* (the truncated receptor polypeptide) acts as a dominant-negative mutant of the *GHSR1a* (functional Ghrelin receptor) due to the formation of *GHSR1a/GHSR1b* heterodimer [16]. The second, a "splicing hypothesis" is that 5'UTR microsatellite ($((TG)_n)$) in the intron affects the efficiency of alternative splicing of an adjacent exon in pre-mRNA (e.g. Cystic fibrosis [17,18] for review). However, this hypothesis seems to have low potential because the *GHSR1a* mRNA is the only spliced mRNA as there are no other alternative splicing variants. Moreover, the position of 5'UTR microsatellite is neither adjacent to 5' splice site (GT) nor 3' splice site (AG) [(GT)-/(111 bases)-/(5'UTR microsatellite)-/(95bases)-/(AG)]. The third, a "translational hypothesis", is more intriguing and interesting as it relates to the differences in RNA secondary structure around the 5'UTR region of the 1b mRNAs between the [19-TG] and [non-19-TG], thus affecting translational levels of 1b mRNAs but not 1a mRNAs. McClelland *et al.* [19] reported that translational efficiency is inversely correlated with the stability of the mRNA secondary structure, the presence of base-pairing in the consensus Kozak sequence, the number of start codons in the 5'UTR and the length of the 5'UTR. In order to test this "translational hypothesis", we predicted the optimal RNA secondary structure of the *GHSR1a* and *GHSR1b* mRNAs using the Vienna RNA secondary structure server (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>; RNA fold web server) [20]. The mRNA sequences of 6 haplotypes (haplotypes frequency: > 0.04) were analyzed. The results showed that the secondary structure around the 5'UTR microsatellite region of the [19-TG]-1b mRNAs had a unique structure that was different from those of [non-19-TG], thus [19-TG] seemed to have a small dominant negative effect on the translation efficiency of *GHSR1b* mRNA due to its unique structure. Therefore, the *GHSR1b* mRNA translation efficiency based on the secondary structure of the 5'UTR microsatellite regions seems to be in the following order: [non-19-TG] $>$ [19-TG]. On the other hand, the optimal RNA secondary structures of the 1a mRNAs appeared to be almost the same among haplotypes and there seemed to be no differences in *GHSR1a* mRNA translation efficiency and *GHSR1a* protein level among these haplotypes. On the basis of these results, we proposed a translational hypothesis that differences in the RNA secondary structure around the 5'UTR region of 1b mRNAs between [19-TG] and [non-19-TG] affect translational levels of 1b mRNAs and the functional Ghrelin receptor level during growth, GH release from the pituitary gland, plasma GH concentration, appetite, glyconeogenesis and finally, growth traits in cattle [9]. This hypothesis should be validated by a molecular biological study in the future.

The *DelR242* in Exon 1 is a 3-bp (AGG) indel (Figure 1). This mutation causes a truncated 3-arginine residue (*3R*) (normal type: 4 arginine residues (*4R*)) of the third loop of the intercellular loop (ICL) domain of the *GHSR1a* protein. The *3R* is a fundamental allele of the *GHSR1a* gene in mice, rats and Chinese hamsters. The *4R* is a fundamental allele in humans, pigs and sheep. Furthermore, in humans, two missense mutations (p.R237W and p.D246A) adjacent to the 4R region of ICL3 of the *GHSR1a* protein have been reported in short-stature families [22,23]. These *GHSR1a* gene mutations displayed a partial loss of constitutive activity in the *GHSR1a* receptor. We found an interesting breed difference in the *3R* allele frequency which was high (0.43) in Japanese Shorthorn and low (0.09) in Holstein-Friesian cattle. This allele was never found in Japanese Black cattle (Figure 1). The *3R* allele is widely distributed in many cattle breeds and may be an older allele than the *4R* allele [8]. The *DelR242* locus and/or the *3R* allele may have some significant effects on growth and feeding behavior in Japanese Shorthorn cattle. To further investigate the reason for a higher frequency of the *3R* allele of the *GHSR1a* gene in Japanese Shorthorn cattle than other cattle breeds, a research project is in progress (manuscript in preparation).

To find a species specific motif within the promoter region of the *GHSR1a* gene in cattle, we compared potential transcriptional regulatory sequences in approximately 2.6 kb of the 5'-flanking region the *GHSR1a* gene among cattle, humans and mice [8]. Six bovine specific motifs were identified as follows: (1) Apolipoprotein E_B1, (2) A-activator binding site (AABS), (3) S1 nuclease-hypersensitive site, (4) Nuclear protein factors and erythroid specific 1_CS1, (5) Nuclear protein factors I, and (6) Nuclear factor_E1. Apolipoprotein E (apoE) is a major constituent of very low density lipoprotein and can be found associated with all of the major classes of lipoprotein particles [24]. Furthermore, AABS motif is a binding site for C/EBP beta (CCAAT/enhancer-binding protein beta) [25]. C/EBP beta is a transcriptional regulator of the UCP1 (uncoupling protein-1) gene, the specific marker gene of brown adipocytes responsible for thermo genic capacity [26]. mRNA expression of the *GHSR1a* gene in cattle may be more coordinated with lipoprotein metabolism than those of humans and mice.

Bovine-specific mRNA expression of the *GHSR1a* gene

Age-related changes in the *GHSR1a* mRNA expression have been reported in rats [27] and in mice [28]. Furthermore, comprehensive tissue distributions of the *GHSR1a* and/or *GHSR1b* mRNA expressions have been reported in humans [29] and in mice [28]. However, in cattle, no comprehensive tissue distributions of the *GHSR1a* and/or *GHSR1b* mRNA expressions in the arcuate nucleus, pituitary gland and other bovine tissues had been reported in cattle. Therefore, in order to develop a better understanding of the age-related functions of *GHSR1a* and *GHSR1b* in the hypothalamus/pituitary-mediated regulation of GH secretion and feeding/growth in cattle, we examined the age-related changes in the *GHSR1a* and *GHSR1b* mRNA expressions in several tissues including the arcuate nucleus and pituitary gland by real-time PCR [30].

Age-related changes in relative expression levels of the *GHSR1a* and *GHSR1b* mRNAs in five tissues including the arcuate nucleus are shown in Table 1. The expression level of *GHSR1a* mRNA in the arcuate nucleus during the post-weaning age was more than 10-fold higher than in pre-weaning calves and the mature cow. The expression level of *GHSR1b* mRNA did not change significantly among age

groups. In the pituitary gland, the expression level of *GHSR1a* and *GHSR1b* mRNAs declined with age.

Age Tissues	GHSR1a mRNA			GHSR1b mRNA		
	Pre-weaning	Post-weaning	Cow	Pre-weaning	Post-weaning	Cow
	Mean (Log ₁₀)*			Mean (Log ₁₀)*		
Arcuate nucleus	0.85	2.14	0.96	0.64	0.31	0.86
Pituitary	1.97	1.01	1.31	1.81	0.73	1.31
Liver	1.11	1.13	0.76	0.05	0.21	0.04
Spleen	0.02	0.09	0.35	0.88	1.85	1.68
Pancreas	-	-0.40	0.29	-	1.72	2.32

Table 1: Age-related changes in relative expression levels of *GHSR1a* and *GHSR1b* mRNAs in several tissues in cattle [30]. *Data are expressed relative to *GAPDH* mRNA {Log₁₀[(copy number of *GHSR1a* mRNA or *GHSR1b* mRNA in 1 µg total RNA / copy number of *GAPDH* mRNA in 1 µg total RNA) 1,000]}. Pre-weaning: 19- to 26-day-old male calves; Post-weaning: 2- to 6.5-month-old steer; Cow: 3.2- to 8.1- year-old cow.

Ghrelin / GHSR stimulate appetite in the arcuate nucleus [1,31]. In the arcuate nucleus, the ghrelin-containing neurons send efferent fibers onto neuropeptide Y (NPY)- and agouti-related protein (AgRP)-expressing neurons to stimulate the release of these orexigenic peptides and onto proopiomelanocortin (POMC) to suppress the release of anorexigenic peptide in rodents [32]. In sheep, offering feed ad libitum (resulting in greater ME intake), decreased hypothalamic mRNA expression of NPY and AgRP and tended to increase that of POMC compared with feed-restricted wethers [33]. The *GHSR1a* mRNA detected in NPY and GHRH neurons in the arcuate nucleus and *GHSR1a* are involved in the up-regulation of NPY and GHRH expression in the arcuate nucleus [34]. In cattle, absolute body weight gain (kg) per month is larger in the post-weaning period than during the pre-weaning phase and adulthood [35]. Voluntary feed intake increases significantly with age and reaches or exceeds 'adult' levels within 6 weeks after weaning [36]. Furthermore, voluntary feed intake per unit of metabolic weight (dry matter (g) / live weight (kg)/ day) from weaning to sexual maturity shows a steady decline with increasing weight [37]. Itoh *et al.* [38] and ThidarMyint *et al.* [39] observed that GH response to ghrelin and growth-hormone-releasing hormone (GHRH) stimulation in post-weaning calves is greater than in pre-weaning calves and cows, but no synergistic effects of ghrelin indicates that in the post-weaning period, the very high expression of *GHSR1a* mRNA and relatively lower expression of *GHSR1b* mRNA in the arcuate nucleus, dramatically amplify ghrelin signaling that stimulates the release of orexigenic peptides (eg, NPY, AgRP, GHRH). These conditions also suppress the release of anorexigenic peptides (eg, -melanocyte stimulating hormone) as well as the secretion of GH in cattle. Therefore, post-weaning calves exhibit a very high voluntary feed intake.

In peripheral tissues, there were 3 marked differences in mRNA expression between cattle (ruminants), humans and mice (monogastric animals), as follows: (1) *GHSR1a* mRNA expression in the liver is high in cattle and very low in humans and mice; (2)

GHSR1b mRNA expression in the liver is low in cattle and high in humans; (3) *GHSR1b* mRNA expression in the pancreas is very high in cattle (Table 2).

Expressi on level	<i>GHSR1a</i>			<i>GHSR1b</i>	
	Cow	Human	Mouse	Cow	Human
High	Pituitary	Pituitary	Pituitary	Pancreas	Myocardium
	Arcuate nucleus	Thyroid	Brain	Spleen	Pituitary
	Liver	Pancreas	Heart	Pituitary	Thyroid
	Spleen	Spleen	Thymus	Arcuate nucleus	Pancreas
	Pancreas	Adrenal	testes	Adipose tissue	Ileum/Colon
	Mammary gland		Lung	Kidney	Liver
	Adipose tissue		Adrenal	Mammary gland	Breast
	Kidney		small intestine	Liver	Spleen
	Heart		spleen	Skeletal muscle	Duodenum
Low	Skeletal muscle		Pancreas	Heart	Placenta

Table 2: Tissue expression levels of *GHSR1a* and *GHSR1b* mRNAs in cow [30], human [29] and mouse [28]. Age: cow, 3.2- to 8.1-year old cow; human, unknown; mouse, 6-wk-old male.

Murata *et al.* [40] reported that *GHSR1a* mRNA is expressed in hepatoma cells and that ghrelin up-regulates the mRNA level of phosphoenolpyruvate carboxykinase (PEPCK), which is the rate-limiting enzyme of gluconeogenesis and modulates downstream molecules involved in insulin-signaling in humans. Furthermore, *GHSR1a* and *ghrelin* mRNAs are expressed in human T lymphocytes and monocytes, where ghrelin acts via *GHSR1a* to especially inhibit the expression of pro-inflammatory anorectic cytokines such as IL-6, IL-1 β and TNF- α [41]. IL-6 is well-known to inhibit the expression of the gluconeogenic genes (phosphoenolpyruvate carboxylase-1(PCK-1) and glucose 6-phosphatase (G6PC)) in the liver via the signal transducer and activator of the transcription-3 (STAT-3) signal cascade [42]. Since hepatic and renal gluconeogenesis is crucially important in glucose metabolism in ruminants [43], the high expression of *GHSR1a* mRNA and the low expression of *GHSR1b* mRNA in the liver seem to be important for gluconeogenesis and represent the bovine-specific expression pattern for maintaining glucose homeostasis in cattle. The very high expression of splenic *GHSR1b* mRNA described may attenuate the inhibition of pro-inflammatory anorectic cytokines and leptin-induced anorectic cytokine expression in monocytes and T cells by the action of ghrelin via *GHSR1a* for maintaining the immune system and appetite control. Ghrelin is expressed in pancreatic islets and there appears to be a negative association between ghrelin and insulin secretion from the pancreas *in vivo* [44]. Ghrelin has been known to function as a potent inhibitor of pancreatic cholecystokinin (CCK)-induced exocrine

secretion in rats [44], and the CCK_A and CCK_B/gastrin receptors, which are G protein-coupled receptors (GPCRs), are expressed in the pancreas in cattle [45]. Moreover, pancreatic polypeptide (PP) is expressed by PP cells in the endocrine pancreas and is released in response to meals as an anorexigenic peptide. A receptor with a high affinity for PP, the Y4 receptor, which is also a GPCR, is expressed in the human pancreas [46]. In addition, the *GHSR1b* and neurotensin receptor 1 (NTSR1) have been shown to be overexpressed in human non-small cell lung cancers (NSCLC), and that a heterodimer complex of these receptors (*GHSR1b*/NTSR1) functioned as a neuromedin U (NMU) receptor. A very high expression of *GHSR1b* mRNA in the pancreas may support the hypothesis that the *GHSR1b* alters the basal expression of *GHSR1a* by the *GHSR1a* - *GHSR1b* heterodimer formation [16]. Furthermore, other GPCRs expressed in the pancreas, such as the CCK_A and CCK_B/gastrin receptors and Y4 receptor, may interact with *GHSR1b* to alter basal expression of these receptors and to ensure a ready response to changes in nutritional / physiological body conditions. Further investigation on the relationship among these receptors is needed.

Bovine-specific nucleotide polymorphisms and mRNA expression of the *GHSR1a* gene described in this mini review will contribute to a better understanding of functions of the *GHSR1a* and *GHSR1b*.

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